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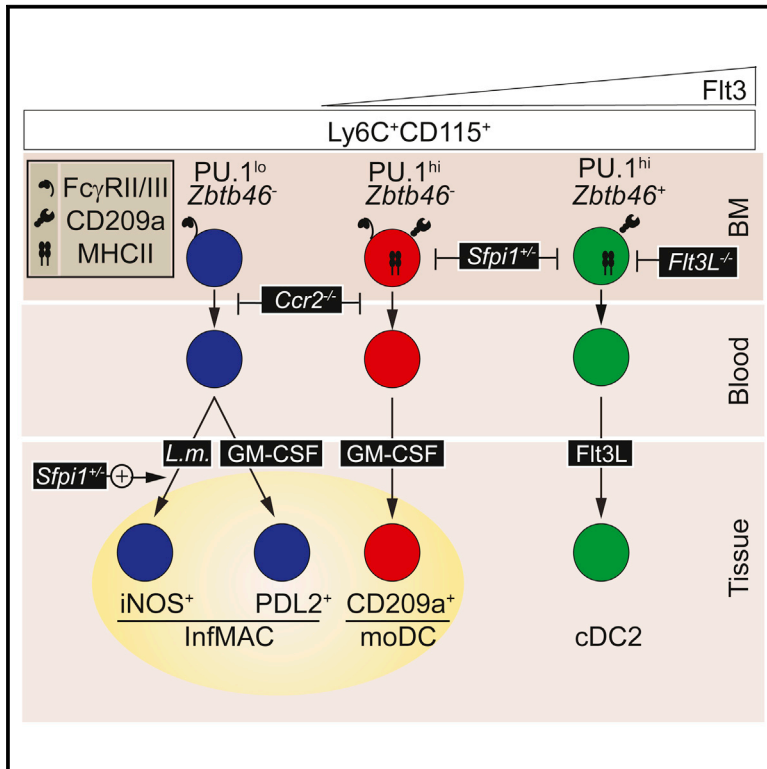
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The Heterogeneity of Ly6C^{hi} Monocytes Controls Their Differentiation into iNOS⁺ Macrophages or Monocyte-Derived Dendritic Cells

Graphical Abstract



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In Brief

Monocytes can differentiate into multiple progenies during inflammation. Here, Menezes et al. show that monocytes from naive mice are heterogeneous and contain distinct precursor subsets giving rise to iNOS⁺ inflammatory macrophages or GM-CSF-induced CD209a⁺ monocyte-derived dendritic cells.

Highlights

- Murine Ly6C^{hi}CD115⁺ monocytes are heterogeneous
- DC-related genes (*Cd209a* and *MHCII*) are expressed in a subset of FcγRIII⁺ monocytes
- GM-CSF-dependent CD209a⁺ moDCs are generated by FcγRIII⁺CD209a⁺MHCII⁺ monocytes
- iNOS⁺ macrophages are generated by FcγRIII⁺CD209a⁻MHCII⁻ monocytes

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The Heterogeneity of Ly6C^{hi} Monocytes Controls Their Differentiation into iNOS⁺ Macrophages or Monocyte-Derived Dendritic Cells

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SUMMARY

Inflammation triggers the differentiation of Ly6C^{hi} monocytes into microbicidal macrophages or monocyte-derived dendritic cells (moDCs). Yet, it is unclear whether environmental inflammatory cues control the polarization of monocytes toward each of these fates or whether specialized monocyte progenitor subsets exist before inflammation. Here, we have shown that naive monocytes are phenotypically heterogeneous and contain an NR4A1- and Flt3L-independent, CCR2-dependent, Flt3⁺CD11c⁺MHCII⁺PU.1^{hi} subset. This subset acted as a precursor for FcγRIII⁺PD-L2⁺CD209a⁺, GM-CSF-dependent moDCs but was distal from the DC lineage, as shown by fate-mapping experiments using *Zbtb46*. By contrast, Flt3⁺CD11c⁺MHCII⁺PU.1^{lo} monocytes differentiated into FcγRIII⁺PD-L2⁺CD209a⁺iNOS⁺ macrophages upon microbial stimulation. Importantly, *Sfp1* haploinsufficiency genetically distinguished the precursor activities of monocytes toward moDCs or microbicidal macrophages. Indeed, *Sfp1*^{+/-} mice had reduced Flt3⁺CD11c⁺MHCII⁺ monocytes and GM-CSF-dependent FcγRIII⁺PD-L2⁺CD209a⁺ moDCs but generated iNOS⁺ macrophages more efficiently. Therefore, intercellular disparities of PU.1 expression within naive monocytes segregate progenitor activity for inflammatory iNOS⁺ macrophages or moDCs.

INTRODUCTION

Haematopoietic stem cells continually give rise to mononuclear phagocytes, including monocytes and conventional dendritic cells (DCs) (Steinman and Cohn, 1973). Both monocytes and DCs arise from common early bone marrow (BM) myeloid progenitors called MDPs (Fogg et al., 2006; Lee et al., 2015). MDPs further differentiate into (1) monocyte-committed progenitors (cMoPs) (Hettinger et al., 2013), giving rise to Ly6C⁺ monocytes unable to differentiate into DCs, and (2) common DC progenitors (CDPs) (Lee et al., 2015; Naik et al., 2007; Onai et al., 2007), which do not give rise to monocytes but generate circulating precursors for DCs (pre-DCs) (Breton et al., 2015; Liu et al., 2009). More recently, MDPs have been shown to generate granulocytes as well (Sathe et al., 2014).

Initially defined by their ability to drive the priming of naive T cells after activation (Nussenzweig et al., 1980), DCs are now regarded as a specific hematopoietic lineage defined by their dependency on growth factor Flt3L (McKenna et al., 2000), which engages the Flt3 receptor tyrosine kinase (CD135) (Waskow et al., 2008), and the expression of the transcription factor (TF) ZBTB46 (Meredith et al., 2012; Satpathy et al., 2012). Fate-mapping (Schraml et al., 2013) and barcoding (Naik et al., 2013) studies have firmly established that DCs are distinct from other lineages.

Monocytes are BM-derived mononuclear phagocytes that circulate in the blood stream. In mice, circulating monocytes are classically defined by expression of CD115 (CSF1R), a receptor for the macrophage growth factor CSF1 (M-CSF). Two categories of monocytes have been identified on the basis of



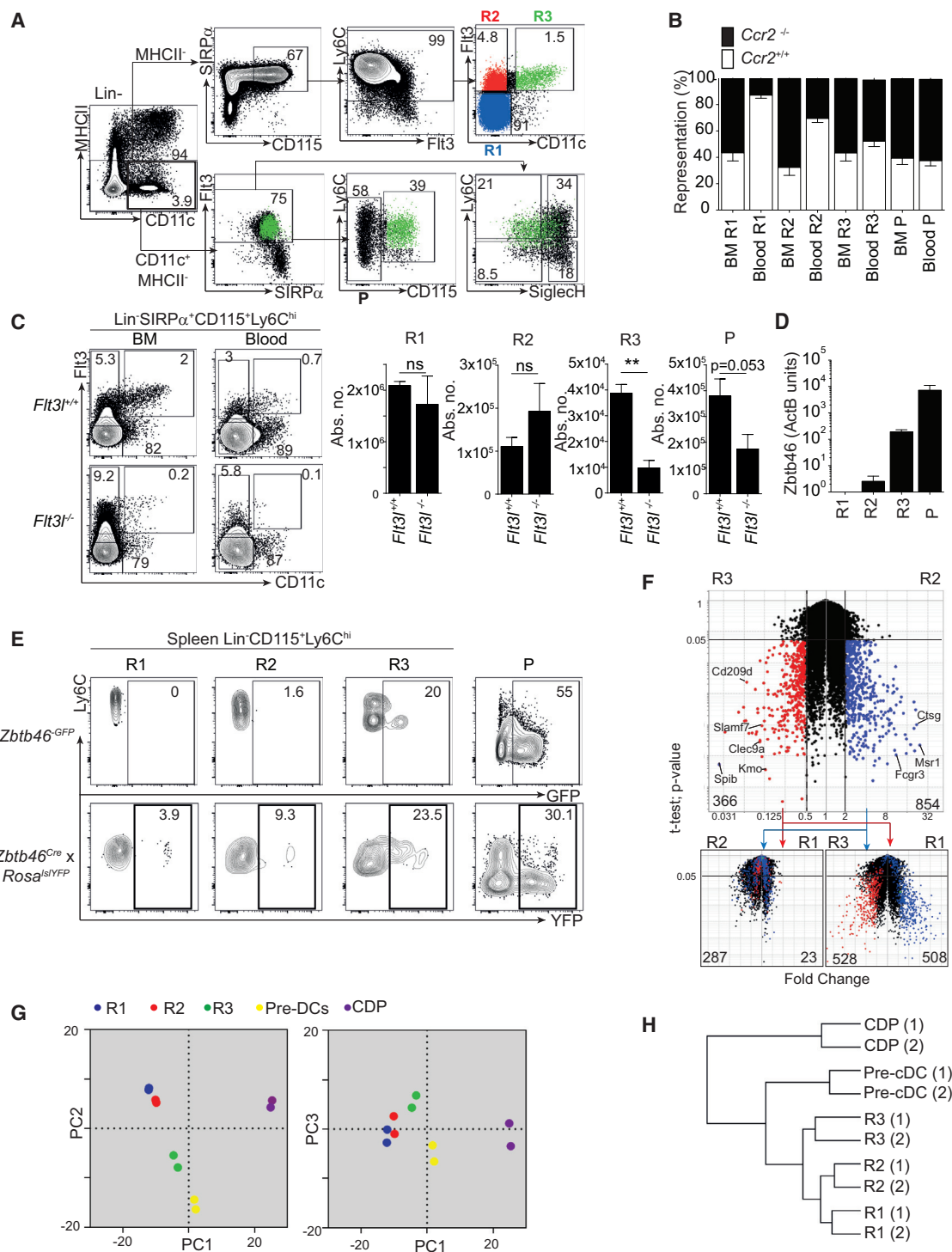


Figure 1. Identification of BM Ly6C⁺CD115⁺ Subsets

(A) BM Lin⁻ MHCII⁻ Ly6C⁺ CD115⁺ monocytes consist of three subsets. Shown is a representative flow cytometry analysis of WT BM at steady state. (Top) Lineage⁻ (CD19⁻, CD3e⁻, Ly6G⁻, Ter119⁻, CD45RA⁻, NK1.1⁻, cKit⁻) MHCII⁻ cells analyzed by a conventional monocyte gating strategy. CD115⁺ Ly6C^{hi} cells can be subdivided into three sub-populations: R1 (Flt3⁺ CD115⁺), R2 (Flt3⁺ CD115⁺), and R3 (Flt3⁺ CD115⁺). (Bottom) Pre-DC gating of Lin⁻ MHCII⁻ CD115⁺ Flt3⁺ SIRPα^{int} cells. Pre-DCs can be subdivided into CD115⁻ (P) and CD115⁺ (R3) subsets. Overlay of R3 is shown in green in the lower panels.

(B) Graphical summary of WT and *Ccr2*^{-/-} mixed BM chimera. Shown are steady-state percentages of WT (CD45.1, white bars) and *Ccr2*^{-/-} (CD45.2, black bars) cells within R1-R3 and P in the BM and blood of WT (CD45.1) reconstituted recipients. Data represent five chimeric mice over two experiments.

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the expression of Ly6C and CX3CR1 according to GFP intensity in *Cx3cr1^{GFP/+}* mice: Ly6C⁺CX3CR1^{int} and Ly6C⁺CX3CR1^{hi} monocytes (Geissmann et al., 2003). Various studies support the notion that Ly6C⁺ monocytes can convert to blood Ly6C⁺ monocytes (Hettinger et al., 2013; Sunderkötter et al., 2004; Varol et al., 2007; Yona et al., 2013). However, selective impairment of Ly6C⁺ monocytes in *Irf8^{-/-}* mutant mice suggests an independent developmental pathway for Ly6C⁺ monocytes (Kurotaki et al., 2013). The egress of BM Ly6C⁺ monocytes at steady state requires the engagement of the chemokine receptor CCR2 (Serbina and Pamer, 2006). By contrast, most Ly6C⁺ monocytes gain access to the bloodstream independently of CCR2 and rely on the TF NR4A1 (Hanna et al., 2012). They exhibit a “patrolling” behavior (Auffray et al., 2007) and scavenge damaged endothelia during inflammation (Carlin et al., 2013). A subset of Ly6C⁺ monocytes expressing extracellular major histocompatibility complex II (MHCII) has also been described (Jakubzick et al., 2013).

Inflammatory monocytes have multiple fates. Pamer and colleagues have elegantly shown that the sensing of *Listeria monocytogenes* (*L.m.*) infection activates the release of CCR2 ligands to mediate the recruitment of Ly6C⁺ monocytes, which differentiate into TNF- α ⁺iNOS⁺ microbicidal phagocytes (Serbina et al., 2003). iNOS⁺Ly6C⁺ phagocytes are distinct from the DC lineage (Meredith et al., 2012; Satpathy et al., 2012) and are essential for the control of *Listeria* infection, as demonstrated by infection of *Nos2^{-/-}* (MacMicking et al., 1995), *Ccr2^{-/-}* (Serbina et al., 2003), and monocyte-depleted (Schreiber et al., 2013) mice.

In addition to differentiating into iNOS⁺ phagocytes, Ly6C⁺ monocytes can differentiate into CCR2-dependent monocyte-derived DCs (moDCs) (Bain et al., 2013; Zigmund et al., 2012). Accordingly, moDCs can be generated upon adoptive transfer of Ly6C⁺ monocytes that progressively lose Ly6C and acquire MHCII when differentiating in inflamed tissues (Bain et al., 2013; Zigmund et al., 2012). Fc γ RI (CD64), Fc ϵ RI, and CD206 have emerged as markers of inflammatory phagocytes distinct from the DC lineage (Cheong et al., 2010; Langlet et al., 2012; Plantinga et al., 2013).

The processes regulating the polarization of Ly6C⁺ monocytes toward iNOS⁺ macrophages or moDCs remain unclear. Local inflammatory cues might control the nature of monocyte progeny. Alternatively, monocyte subpopulations might be endowed with a selective potential to generate iNOS⁺ phagocytes or moDCs. Here, we report the description and functional characterization of monocyte subsets endowed with the selective ability to generate iNOS⁺ phagocytes or moDCs. We show that the

amount of PU.1 arbitrates the commitment of monocytes toward either cell fate.

RESULTS

Ly6C⁺ Monocytes Are Heterogeneous

As an initial approach to addressing the heterogeneity of BM mononuclear phagocyte precursors, we analyzed the expression of CD135 (Flt3) and CD115 (CSF1R) in Lin⁺ BM cells (Figure 1A; isotype controls in Figure S1A). MHCII⁺ cells were not considered because they correspond to F4/80^{hi} BM macrophages (Figure S1B). We noticed that MHCII⁺CD172a (SIRP α)⁺CD115⁺Ly6C⁺ cells contained three sub-populations: a major CD11c⁺Flt3⁺ (R1) and two minor CD11c⁺Flt3⁺ (R2) and CD11c⁺Flt3⁺ (R3) populations (Figures 1A and S1C). R3 corresponded phenotypically to a subset of pre-DCs (CD11c⁺Flt3⁺SIRP α ^{int}; Liu et al., 2009; Figure 1A) and was distinct from cKit⁺CD115⁺Flt3⁺ CDPs (Naik et al., 2007; Onai et al., 2007; Figure S1D). Within pre-DCs, R3 coexisted with CD115⁺ pre-DCs (P) and aligned with both the Ly6C⁺SiglecH⁺ and Ly6C⁺SiglecH⁺ pre-DC subsets (Figure 1A; Schlitzer et al., 2015). R1 and R2 monocytes expressed heterogeneous amounts of CD11b and CX3CR1 (Figure S1E), had horse-shoe-shaped nuclei (Figure S1F), and were distinct from *Nr4a1*-dependent Ly6C^{lo} monocytes (Figure S1G).

Blood Lin⁺CD115⁺Ly6C⁺ cells, like their Ly6C⁺ BM counterparts, also contained sub-populations R1–R3 (Figures 1B and 1C). R1 expressed higher amounts of CCR2 than R2 and R3 (Figure S1E), and *Ccr2* inactivation drastically restricted the size of circulating R1 and R2 monocytes, but not pre-DCs (Figure S1H). Mixed BM chimeras of wild-type (WT) and *Ccr2^{-/-}* cells showed that CCR2 controls the egress of R1 and R2 monocytes by a cell-intrinsic effect (Figures 1B and S1I).

Unlike pre-DCs and DCs (McKenna et al., 2000), BM and blood R1 and R2 cells were largely independent of growth factor Flt3L (Figure 1C). The DC-specific TF-encoding gene *Zbtb46* (BTBD4) was highly expressed only in R3 and P pre-DCs (Figure 1D). Accordingly, reporter expression in *Zbtb46^{GFP/+}* mice and fate mapping in the *Zbtb46^{Cre} x Rosa^{slYFP}* model (Loschko et al., 2016; Figures 1E and S1J) showed that splenic R3 and P pre-DCs, but not R1 or R2 monocytes, belonged to the DC lineage.

Genes with higher expression in R3 pre-DCs than in R2 monocytes largely overlapped the genes with higher expression in R3 pre-DCs than in R1 monocytes (e.g., *Clec9a* and *Slamf7*; Figure 1F, red dots; Table S1) and, to a lesser extent, overlapped genes with higher expression in R2 monocytes than in R1 monocytes (*Ctsg* and *Flt3*; Figure 1F, red dots in lower left plot). R3

(C) Flow cytometry analysis of R1–R3 and P in *Flt3l^{-/-}* and *Flt3l^{+/+}* BM and blood. Quantification shows the absolute number of each cell population within the blood (n = 4 mice per group).

(D) qPCR for *Zbtb46* in WT BM R1–R3 and P in β -actin units.

(E) *Zbtb46* labeling and reporter expression. Steady-state GFP reporter expression and YFP expression in splenic R1–R3 and P cells in *Zbtb46^{GFP/+}* and *Zbtb46^{Cre} x Rosa^{slYFP}* mice, respectively.

(F) Genes differentially expressed among R1–R3. Volcano plots of R2 versus R3 (main plot) show genes with a fold change ≥ 2 and a p value of $p < 0.05$ in R2 (blue) and R3 (red). These genes are overlaid on volcano plots of R1 versus R2 (left) and R1 versus R3 (right) with the same axes of fold change and p value. Numbers indicate differentially expressed genes in each comparison (gene list available in Table S1).

(G) Clustering of R1–R3 with pre-DCs and CDPs. Principal-component analysis compares microarray data of R1 (blue), R2 (red), and R3 (green) with previously published data of pre-DCs (yellow) and CDPs (violet) on PC1 (72% variance), PC2 (24% variance), and PC3 (2% variance).

(H) Hierarchical clustering analysis (1 – Pearson correlation) of monocytes (R1 and R2), pre-DCs (R3), total pre-DCs, and CDPs.

Data represent the mean \pm SEM (* $p < 0.05$; ** $p < 0.005$; ns, not significant; Student's t test). Please also refer to Figure S1.

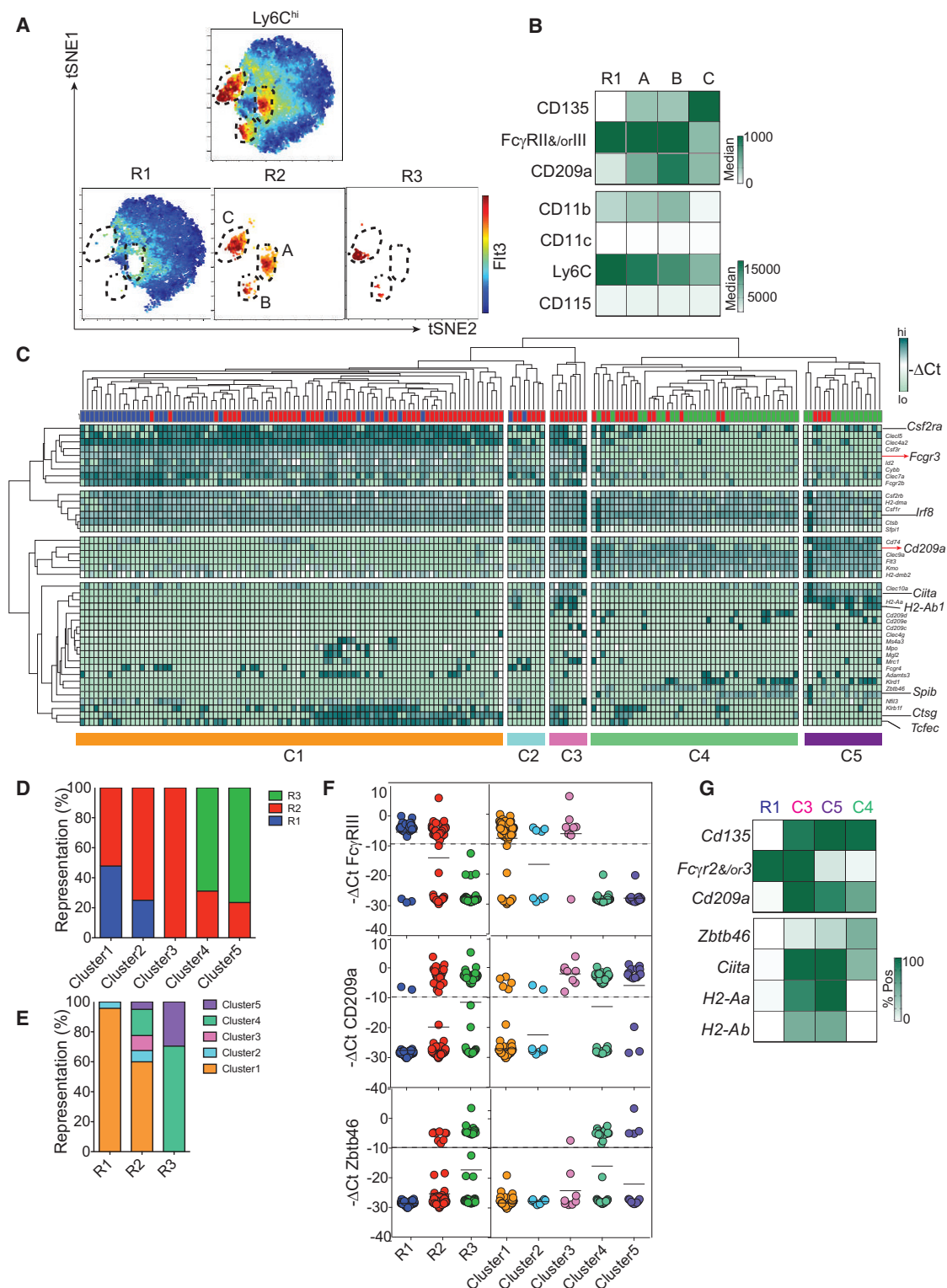


Figure 2. Transcriptional Profiling of Monocyte Subsets R1 and R2

(A) Nonlinear dimensionality reduction analysis of $\text{Ly6C}^{\text{hi}}\text{CD115}^{\text{+}}\text{SIRP}\alpha^{\text{+}}$ cells. t-SNE maps of total $\text{Lin}^{\text{+}}\text{MHCII}^{\text{+}}\text{CD115}^{\text{+}}\text{SIRP}\alpha^{\text{+}}$ cells, R1 and R2 monocytes, and R3 pre-DCs are based on the parameters CD115, SIRP α , Ly6C, Flt3, CD11c, CD209a, and Fc γ RII and/or Fc γ RIII. Color scale indicates Flt3 expression.

(B) Expression analysis of t-SNE-generated sub-populations of R2 and expression of Flt3, Fc γ RII and/or Fc γ RIII, CD209a, CD11b, CD11c, Ly6C, and CD115 of t-SNE-generated Flt3 $^{\text{+}}$ populations A–C with R1 monocytes. CD209a expression is shown as the difference between MFI and fluorescence minus one (FMO) control for all four populations.

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pre-DCs expressed genes belonging to the DC signature (Miller et al., 2012) (e.g., *Clec9a* and *Slamf7*; Figures 1F and S1K) and clustered with total pre-DCs and CDPs (Figures 1G and 1H).

Genes with higher expression in R2 monocytes than in R3 pre-DCs (Figure 1F, blue dots in the main panel) largely overlapped the genes with higher expression in R1 monocytes than in R3 pre-DCs (e.g., *Msr1* and *Fcgr3*; Figure 1F, lower right plot; Table S1). However, most of these genes were not differentially expressed between R2 and R1 monocytes (Figure 1F, blue dots in lower left panel). Furthermore, R1 and R2 expressed a macrophage signature (e.g., *Fcgr3* and *Csf3r*; Figure S1K; Gautier et al., 2012) while clustering close to each other (Figures 1G and 1H) apart from the DC-committed precursors.

Overall, R1 and R2 were more similar to each other than to R3 (Figures 1F–1H; Table S1). We conclude that R1 and R2 qualify as bona fide monocytes given that both are largely CCR2 dependent for BM egress, do not rely on *Flt3L*, and do not express *Zbtb46*. R3 met all the criteria for bona fide pre-DCs because it was largely CCR2 independent and *Flt3L* dependent and expressed the DC-specific *Zbtb46* (Meredith et al., 2012; Satpathy et al., 2012).

R2 Monocytes Bear a Mixed Transcriptional Profile

We next aimed to assess the diversity of *Ly6C*⁺ monocytes by using unsupervised analyses. To this end, we used multi-dimensional reduction analysis of multi-parametric flow cytometry. BM *Ly6C*⁺*CD115*⁺ cells were divisible into one major *Flt3*⁺ and three minor *Flt3*⁺ subsets with distinct t-distributed stochastic neighbor embedding (t-SNE) coordinates (populations A–C) (Figure 2A). Population A was *CD11c*⁺ and found only within R2. By contrast, populations B and C overlapped R2 and R3. Unlike population C, A and B phenotypically shared high expression of *FcγRIII* and/or *FcγRIIIb* with R1 monocytes. However, like population C but unlike R1 monocytes, A and B expressed *CD209a* (Figure 2B). All together, these data were corroborated by microarray analysis of BM R1–R3 populations (Figure S2A) and flow cytometry analysis of blood *Ly6C*⁺ cells (Figure S2B). In addition, population C had lower *CD11b* expression than A and B (Figure 2B).

As a parallel unsupervised approach, we used gene-expression profiling at the single-cell level to assess the diversity of *Ly6C*⁺*CD115*⁺ cells. We performed single-cell qPCR by using a set of 42 genes and 3 house-keeping controls. Unsupervised clustering of gene expression at the single-cell level revealed the existence of five clusters within *Ly6C*⁺*CD115*⁺ cells (Figure 2C). Clusters 1 and 2 aligned mostly with R1 and also partially with R2. Cluster 3 was exclusively represented within R2, whereas clusters 4 and 5 were enriched in R3 but also present in R2 (Figures 2C–2E). Cluster 3 was unique in its mixed expression pattern of monocyte (*Fcgr3*, *Fcgr2b*, and *Csf3r*) and DC

(*Kmo*, *Cd209a*, and *Flt3*) genes (Figures 2C and 2F and S2A and S2B). However, cluster 3 (in addition to clusters 1 and 2) showed low transcription of *Zbtb46*, which was found in clusters 4 and 5 (Figure 2F).

Of interest, we noticed that the expression of *Ciita* and MHCII-related genes was found mostly in clusters 3 and 5 (Figure S2C). This is consistent with MHCII expression in BM and blood R2 and R3, as assessed by flow cytometry and microarray analysis (Figures S2D and S2E). R2 and R3 thus aligned with previously described *Ly6C*⁺*CD115*⁺MHCII⁺ cells in the blood (Carlin et al., 2013; Jakubczik et al., 2013; Figure S2F). Using mice deficient of various CIITA promoters (*pl*^{−/−}, *pIV*^{−/−}, or *plII*⁺*pIV*^{−/−}), we showed that R2, like DCs, expressed MHCII after *pl*-dependent induction of *Ciita* (LeibundGut-Landmann et al., 2004; Figures S2G and S2H).

All together, both unsupervised flow cytometry and gene-expression analyses revealed that R2 monocytes contained unique populations of *Zbtb46*[−] cells that were distinct from the cDC lineage and expressed transcriptional profiles with mixed features of monocytes and cDCs (*Zbtb46*[−] *Flt3*⁺*FcγRIII* and/or *FcγRIII*⁺*CD209a*⁺*CD11c*[−]). Using MHCII as a surrogate marker for these cells, we showed that they are independent of *Flt3L* and rely on CCR2 for their mobilization from the BM to the blood (Figures S2I and S2J).

PU.1 Controls the Formation of *Flt3*⁺MHCII⁺ R2 Monocytes

We next sought to identify TFs regulating the formation of R2 *Flt3*⁺MHCII⁺ monocytes. *Sfp1* (PU.1) is an attractive candidate because it promotes *Flt3* expression (Carotta et al., 2010) and MHCII through the induction of *Ciita* (Bakri et al., 2005). Intracellular flow cytometry staining for PU.1 indicated that R3 pre-DCs and R2 monocytes expressed higher amounts of PU.1 than R1 monocytes (Figure 3A). Accordingly, PU.1 was expressed more in MHCII⁺ than in MHCII[−] blood *CD115*⁺ cells (Figure 3B).

The effects of PU.1 were tightly dependent on its expression; therefore, we analyzed *Sfp1*^{+/−} mice that had reached adulthood without any obvious phenotype. *Sfp1*^{+/−} mice had reduced numbers of blood *CD115*⁺*Ly6C*^{lo} cells, whereas blood *Ly6C*⁺ were not affected despite an increase in BM *Ly6C*⁺ cells (Figure 3C). *Sfp1*^{+/−} mice had reduced MHCII⁺ (*Ly6C*⁺ and *Ly6C*[−]) *CD115*⁺ populations in the BM and blood (Figure 3D). Finally, *Sfp1*^{+/−} mice had smaller populations of R2 monocytes (including the MHCII⁺ fraction of R2) and R3 pre-DCs than WT mice in BM and blood (Figures 3E and S3A–S3C). In agreement with R3 pre-DC reduction, *Sfp1*^{+/−} mice displayed a selective deficiency in spleen *CD11b*⁺ DCs, mostly in the ESAM1^{lo}*Flt3*^{lo} compartment, whereas plasmacytoid DCs remained unchanged (Figures S3D–S3F). In contrast to R2 monocytes and R3

(C) Heterogeneity in population R2. The hierarchical clustering dendrogram (top and left margins) is based on $-\Delta Ct$ values from single-cell multiplex qPCR analysis of 44 R1 (blue), 81 R2 (red), and 44 R3 (green) single cells for 42 genes.

(D) Representation of populations R1–R3 within the five clusters defined in (C).

(E) Representation of the five clusters within populations R1–R3.

(F) Single-cell expression of *Fcgr3*, *CD209a*, and *Zbtb46* in populations R1–R3 or clusters C1–C5. Each dot represents the $-\Delta Ct$ value of a single cell.

(G) Analysis of the defining genes of population R1 with clusters C3–C5. The heatmap compares mRNA expression of MHCII-related genes *Cd135*, *Zbtb46*, *Cd209a*, and *Fcgr2* and/or *Fcgr3* on single cells between clusters C3–C5 and monocyte population R1.

Please also refer to Figure S2.

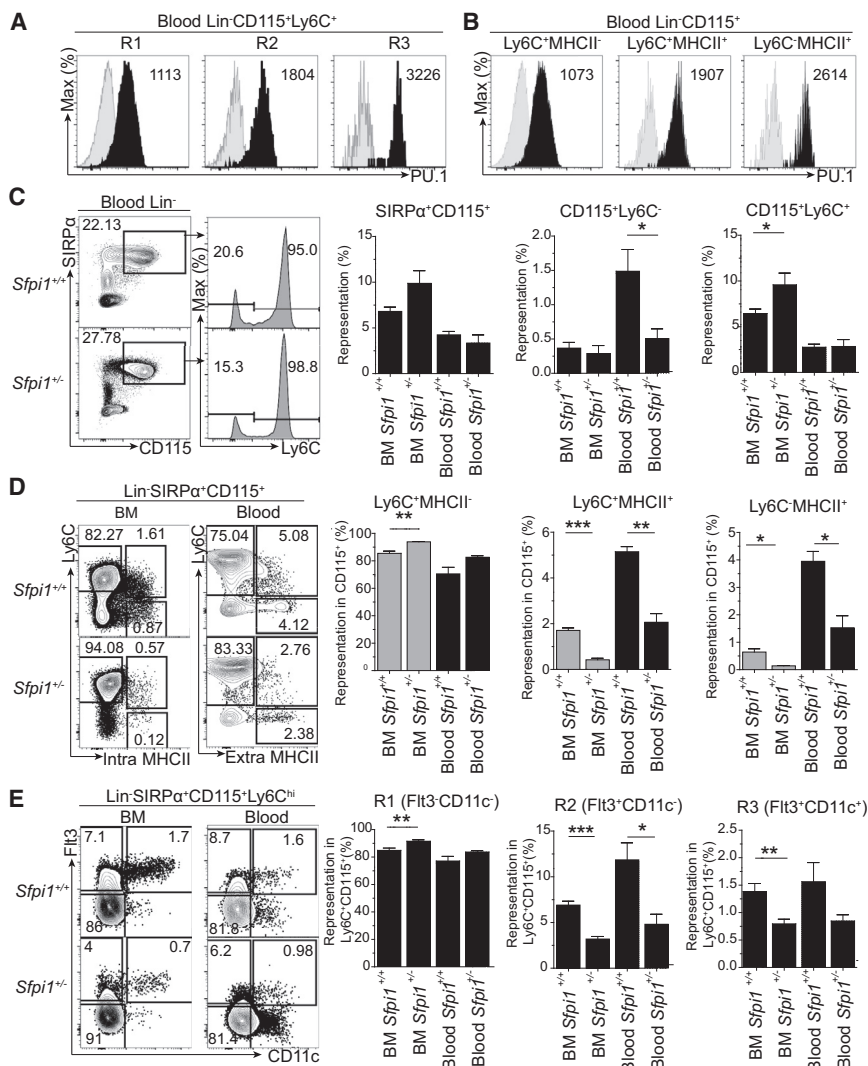


Figure 3. PU.1 Controls the Development of PU.1^{hi}Fli3⁺MHCII⁺ R2 Monocytes at Steady State

(A and B) Expression of PU.1 (black shading) and isotype control (gray shading) within Ly6C^{hi}CD115⁺ monocytes (R1 and R2) and pre-DCs (R3) (A) and in Ly6C^{hi}MHCII⁻, Ly6C^{hi}MHCII⁺, and Ly6C⁻MHCII⁺ cells (B) in the blood as seen by intra-nuclear staining of PU.1 by flow cytometry. Numbers within plots indicate the MFI of PU.1.

(C–E) Representative flow cytometric analysis of the blood of *Sfp1*^{+/+} and *Sfp1*^{-/-} mice at steady state. (C) Comparison of total (SIRPα⁺CD115⁺), Ly6C⁺, and Ly6C^{lo} blood monocytes by flow cytometry and quantification as the percentage of total live cells. (D and E) Comparison of Ly6C⁺MHCII⁻, Ly6C⁺MHCII⁺, and Ly6C⁻MHCII⁺ cells within SIRPα⁺CD115⁺ monocytes (D) and of R1–R3 within Ly6C^{hi}MHCII^{+/−} monocytes (E) in the BM and blood. Gray bars indicate intracellular staining for MHCII.

Data represent the mean ± SEM of three mice per group from three identical experiments (*p < 0.05, **p < 0.005, ***p < 0.0005; Student's t test). Please also refer to Figure S3.

pre-DCs, R1 monocytes were slightly increased in the BM of *Sfp1*^{+/−} mice (Figure 3E). However, this increase did not reach significance in the blood (Figures 3E, S3A, and S3B). *Sfp1* hemizygosity reduced the numbers of MDPs and CDPs, but not cMoPs (Figure S3F). We conclude that high expression of PU.1 is selectively required for the development of Fli3⁺MHCII⁺ R2 monocytes and R3 pre-DCs at steady state.

PU.1^{lo}Fli3⁺MHCII⁺ R1 Monocytes Generate iNOS⁺ Macrophages upon Microbial Stimulation

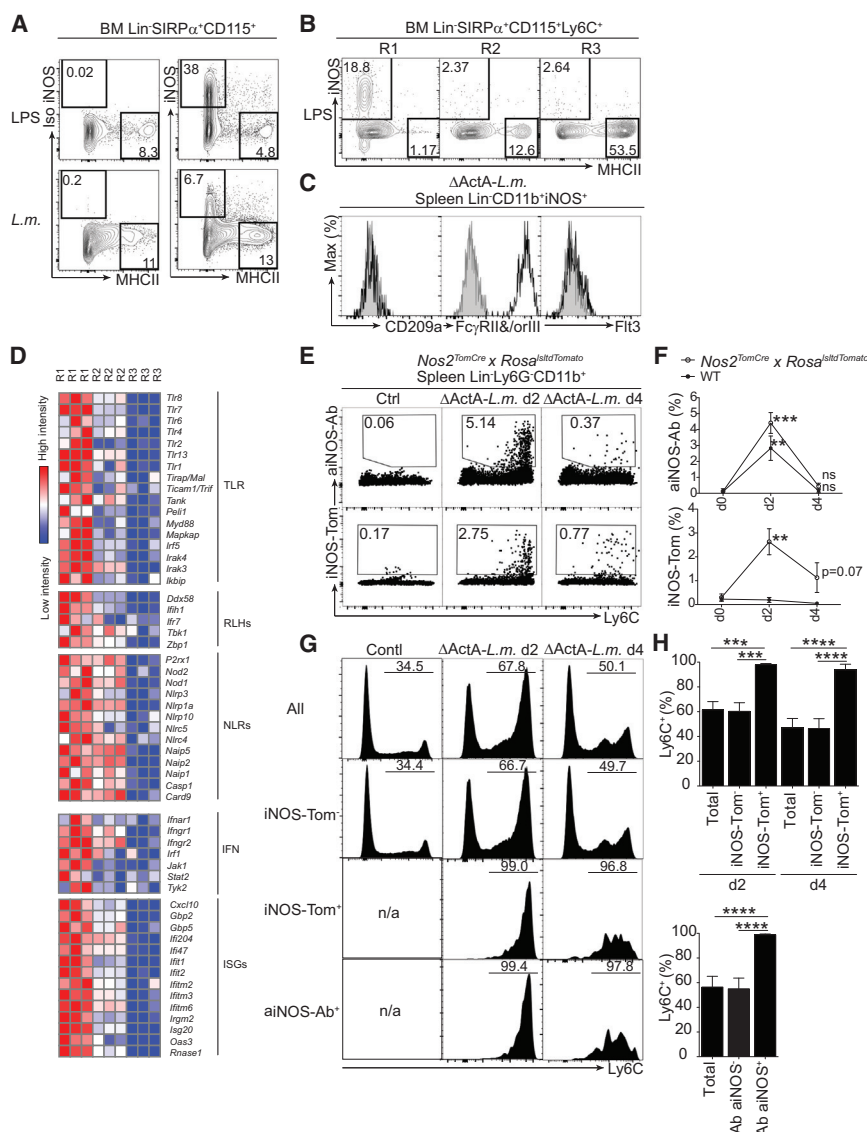
In the next set of experiments, we aimed to determine which Ly6C⁺ monocytes are precursors for iNOS⁺ macrophages. We chose to use *Listeria* infection because it efficiently induces the recruitment and differentiation of iNOS⁺ phagocytes from Ly6C⁺ monocytes (Serbina et al., 2003). In agreement with their independence of Fli3L (Meredith et al., 2012), *L.m.*-induced iNOS⁺ macrophages were not identified in *Zbtb46*^{cre}*xROS*^{lsYFP} mice (Loschko et al., 2016), thus confirming their monocytic origin (Figure S4A). In vitro exposure to lipopolysaccharide (LPS) or infection with *L.m.* resulted in iNOS expression in a subset of responding BM CD115⁺Ly6C⁺ cells (up to 38%) that

remained mostly MHCII^{lo} (Figure 4A), unless these cells were treated with interferon-γ (IFN-γ), which increased MHCII expression in iNOS⁺ cells (Figure S4B). Overnight culture of sorted R1 or R2 monocytes or R3 pre-DCs with *L.m.* or LPS (Figures 4B and S4C) revealed the selective ability of R1 to produce iNOS⁺ MHCII⁺ macrophages, whereas R2 and R3 generated iNOS⁺MHCII⁺ cells (Figures 4B and S4C). We conclude that the formation of iNOS⁺ macrophages upon

microbial exposure is a selective feature of R1 monocytes or possibly a subset of them. Like R1 monocytes (Figures 2F and 2G), in-vivo-generated Ly6C⁺CD11b⁺iNOS⁺ macrophages (Serbina et al., 2003) expressed FcγRII and/or FcγRIII, but not CD209a or Fli3 (Figure 4C).

Transcriptomic analysis of BM R1–R3 demonstrated an upregulation of toll-like receptor (TLR) signaling, RIG-like helicase, NOD-like receptor genes, and IFN-γ signaling and its target genes in R1 monocytes (Figure 4D). We conclude that R1 cells are efficiently equipped for innate sensing prior to microbial exposure.

We next wanted to determine whether iNOS⁺ macrophages lose iNOS and enter a differentiation pathway of monocytes characterized by the loss of Ly6C in inflamed tissues (Bain et al., 2013; Zigmond et al., 2012). We used a fate-mapping approach to irreversibly label iNOS-expressing cells in *Nos2*^{tomato-cre}*xROS*^{lsYFP} mice. *L.m.* infection triggered the labeling (Tomato⁺) of a subset of Ly6C⁺ cells 2 days after infection; these cells were also stained with anti-iNOS antibody (Figures 4E, 4F, and S4D). We found that by day 4, the iNOS⁺ cells (both Tomato⁺ and anti-iNOS-Ab⁺ cells) had reduced drastically



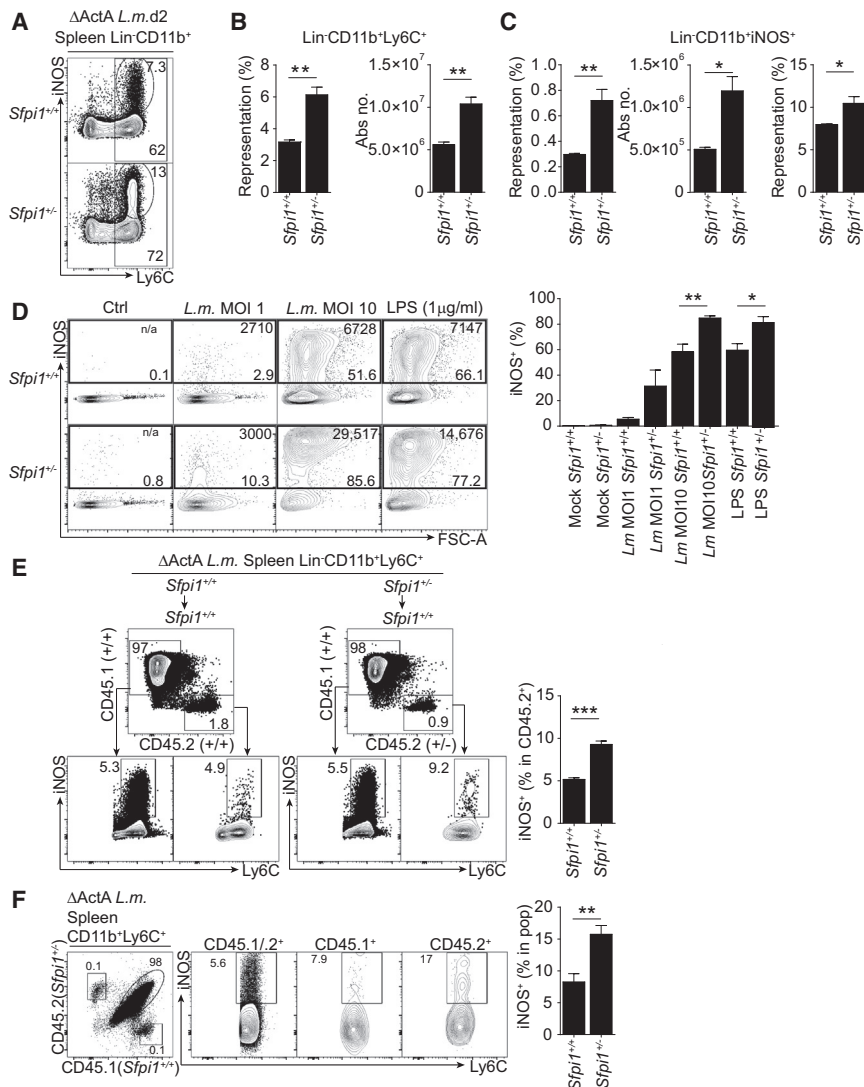


Figure 5. PU.1 Inhibits the Generation of iNOS⁺ Macrophages upon Microbial Stimulation

(A–C) Generation of Ly6C⁺iNOS⁺ cells upon microbial stimulation of *Sfp1*^{+/+} or *Sfp1*^{+/-} mice. (A) Intracellular flow cytometry staining of spleen Lin⁺ (CD19⁺, CD3e⁺, Ly6G⁺, Ter119⁺, CD45RA⁺, NK1.1⁺, cKit⁺) CD11b⁺ cells in *Sfp1*^{+/+} and *Sfp1*^{+/-} mice infected with Δ ActA *L.m.* (B and C) Quantification of the percentage and absolute number of Lin⁺CD11b⁺Ly6C⁺ cells (B) and Lin⁺CD11b⁺iNOS⁺ cells (C).

(D) Microbial stimulation of BMDMs generated from *Sfp1*^{+/+} or *Sfp1*^{+/-} mice and flow cytometry analysis of iNOS⁺ BMDMs from *Sfp1*^{+/+} and *Sfp1*^{+/-} mice. BMDMs were cultured with MCSF alone, MCSF and *L.m.* at a MOI of 1 or 10, or MCSF and 1 μ g/ml LPS. Numbers at the top of each gate indicate MFI. The percentage of iNOS⁺ cells obtained within each culture is quantified.

(E) PU.1 reduction in the BM compartment results in an increase in iNOS⁺ macrophages in vivo. CD45.2⁺*Sfp1*^{+/+} or *Sfp1*^{+/-} whole BM was adoptively transferred into WT Δ ActA *L.m.*-infected CD45.1⁺ recipients. Representative flow cytometry analysis of iNOS expression in Lin⁺CD11b⁺Ly6C⁺ splenocytes from recipients (CD45.1⁺) or donors (CD45.2⁺) is shown.

(F) PU.1 in monocytes regulates the production of iNOS⁺ macrophages in vivo. Shown is flow cytometry analysis of iNOS expression in Lin⁺CD11b⁺Ly6C⁺ cells of CD45.1⁺*Sfp1*^{+/+} and CD45.2⁺*Sfp1*^{+/-} sorted BM monocytes adoptively transferred intravenously into WT Δ ActA *L.m.*-infected CD45.1/2⁺ recipients (n = 4 mice per group).

Data represent the mean \pm SEM (*p < 0.05; **p < 0.005; ***p < 0.0005; ns, not significant; Student's t test). Please also refer to Figure S5.

(Figure 5E). Finally, to address the role of *Sfp1* in the monocyte compartment, we engrafted a mixture of *Sfp1*^{+/-} (CD45.2) and *Sfp1*^{+/+} (CD45.1) BM monocytes into *L.m.*-infected CD45.1 and CD45.2 recipient mice. We found that the percentage of iNOS⁺ macrophages within Ly6C⁺CD11b⁺ cells was higher in the progeny of *Sfp1*^{+/-} monocytes than in that of *Sfp1*^{+/+} monocytes (Figure 5F).

We conclude that PU.1 acts as a cell-intrinsic negative regulator of the differentiation of monocytes into iNOS⁺ macrophages upon microbial exposure.

PU.1^{hi}Flt3⁺MHCII⁺ R2 Monocytes Differentiate into PDL2⁺CD209a⁺ moDCs upon GM-CSF Exposure

Having established that R1 monocytes are poised to generate iNOS⁺ macrophages, we next assessed the ability of monocyte subsets to give rise to moDCs. Elevation of granulocyte-macrophage colony-stimulating factor (GM-CSF) concentrations induces the accumulation of CD11b⁺MHCII⁺ spleen cells that resemble CD11b⁺ DCs (Daro et al., 2000; Mach et al., 2000). Engraftment of live GM-CSF-producing B16

melanoma (B16-GM-CSF) (Dranoff et al., 1993) triggered the expansion of (1) circulating MHCII⁺ monocytes with varying expression levels of Ly6C (Figure S6A) and (2) Lin⁺Ly6G⁺CD11b⁺Ly6C^{hi-lo}MHCII⁺ spleen cells largely overlapping the CD11b⁺ DC phenotype (Figure S6B). GM-CSF-induced (or LPS-induced; Figure S6C) Ly6C^{hi-lo}MHCII⁺ cells can be subdivided according to their expression of Fc γ RII and/or Fc γ RIII and CD209a (Figures 6A and 6B). Both CD209a⁺ and CD209a⁺ Fc γ RII⁺ and/or Fc γ RIII⁺ populations rely on CCR2 (Figure S6D). Compared with CD4⁺ DCs, CD209a⁺ and CD209a⁺ Fc γ RII⁺ and/or Fc γ RIII⁺ cells expressed greater CD115 and lower Flt3 and ESAM1 (Figures 6B and S6E). In stark contrast with CD4⁺CD11b⁺ DCs (Figures 6B and S6E), both expressed PD-L2 and low amounts of PD-L1 (Figures 6B and S6C). Additionally, both CD209a⁺ and CD209a⁺ Fc γ RII⁺ and/or Fc γ RIII⁺ cells had lower expression of YFP than CD4⁺ DCs from naive or B16-GM-CSF-bearing *Zbtb46*^{Cre} \times *Rosa*^{lsYFP} mice (Loschko et al., 2016; Figures 6B and S6F). A similar hierarchy of labeling was obtained in the *Zbtb46*^{GFP/+} reporter mice (Satpathy et al., 2012;

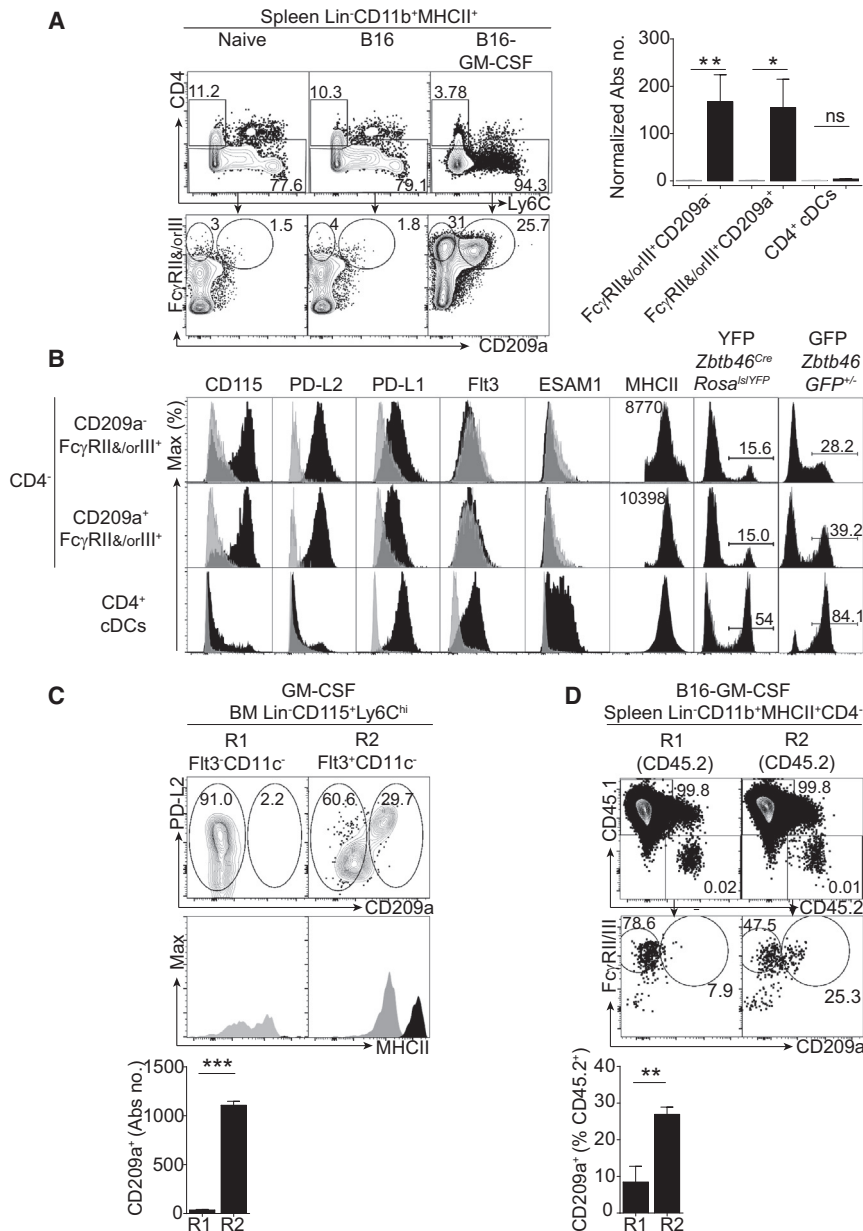


Figure 6. PU.1^{hi}Fli3⁺MHCII⁺ R2 Monocytes Differentiate into PD-L2⁺CD209a⁺ moDCs upon Exposure to GM-CSF

(A) Phenotype of spleen cells from control, B16, or B16-GM-CSF-engrafted mice. FACS analysis for CD4, Ly6C, FcγRII and/or FcγRIII, and CD209a expression within Lin⁻ (Ly6G⁻, CD3e⁻, NK1.1⁻, Ter119⁻, CD45RA⁻, cKit⁻) CD11b⁺MHCII⁺ spleen cells in naive, B16, or B16-GM-CSF-bearing mice. Absolute numbers of CD4⁺FcγRII⁺ and/or FcγRIII⁺CD209a⁻, CD4⁺FcγRII⁺ and/or FcγRIII⁺CD209a⁺, and CD4⁺ cells in Lin⁻CD11b⁺MHCII⁺ cells in spleens from B16-GM-CSF-engrafted mice. Data are normalized to the naive control of each population.

(B) Phenotype of CD4⁺FcγRII⁺ and/or FcγRIII⁺CD209a⁻, CD4⁺FcγRII⁺ and/or FcγRIII⁺CD209a⁺, and CD4⁺ cells in Lin⁻Ly6G⁻CD11b⁺MHCII⁺ splenocytes from B16-GM-CSF-bearing mice. Extracellular flow cytometry analysis of each population is shown for CD115, PDL2 (CD273), PDL1 (CD274), Fli3, ESAM1, and MHCII (black) against isotype controls (gray). YFP labeling of the indicated populations in *Zbtb46*^{Cre} × *Rosa*^{lsYFP} mice and GFP labeling in *Zbtb46*^{GFP/+} mice is also shown. Numbers above the histograms indicate MFI. Data represent five mice over two experiments.

(C) GM-CSF culture of flow-cytometry-sorted R1 and R2 BM monocytes. Shown is PDL2 and CD209a expression on DAPI⁺CD45⁺ cells after 2 days of culture and MHCII expression of CD209a⁻ (gray) and CD209a⁺ (black). Data represent three independent cultures.

(D) Cell fate of flow-cytometry-sorted R1 and R2 BM monocytes adoptively transferred into B16-GM-CSF-engrafted mice. Shown is FcγRII and/or FcγRIII and CD209a expression on recipient CD45.1⁺ (Figure S6G) and donor CD45.2⁺ cells in the spleens of CD45.1⁺ B16-GM-CSF-bearing recipients, as well as quantification of CD209a⁺ cells within Lin⁻CD11b⁺MHCII⁺CD4⁺CD45.2⁺ cells. Data represent the mean ± SEM (*p < 0.05; **p < 0.005; ***p < 0.0005; ns, not significant; Student's t test). Please also refer to Figure S1.

Figure 6B). Together, these results support a monocytic origin of CD209a⁻ and CD209a⁺ FcγRII⁺ and/or FcγRIII⁺ cells.

Finally, we addressed whether R1 and/or R2 BM monocytes could differentiate into PDL2⁺CD209a⁺ cells upon short-term culture in GM-CSF. We found that, reminiscent of macrophages produced during long-term GM-CSF culture (Barthélemy et al., 2015), R1 cells produced exclusively CD209a⁻MHCII^{lo}PDL2⁺ cells. Unlike R1, R2 monocytes produced CD209a⁺MHCII^{hi}PDL2⁺ cells (Figure 6C). In vivo, adoptive transfer of R2, but not R1, monocytes in B16-GM-CSF-engrafted mice generated CD209a⁺ moDCs, as was seen in the CD45.1⁺ recipients (Figures 6D and S6G). We conclude that R2, but not R1, monocytes exhibit a precursor ability for CD209a⁺PDL2⁺ moDCs in vitro and in vivo.

An Increase in PU.1 Promotes the Generation of Monocyte-Derived PDL2⁺CD209a⁺ moDCs

Finally, we investigated whether a higher expression of PU.1 is required for the differentiation of GM-CSF-induced moDCs. The generation of PD-L2⁺CD86^{hi}MHCII^{hi} moDCs (Barthélemy et al., 2015; Gao et al., 2013) from BM GM-CSF cultures was lower in *Sfp1*^{+/-} cultures than in WT cultures (Figure S7A). WT, but not *Sfp1*^{+/-} Ly6C^{hi}, monocytes generated PD-L2⁺CD209a⁺ moDCs in vitro (Figure 7A). Analyzing B16-GM-CSF-engrafted *Sfp1*^{+/-} or *Sfp1*^{+/-} mice, we found that the expansion of CD209a⁺ moDCs (but not FcγRII⁺ and/or FcγRIII⁺ CD209a⁻ macrophages) was selectively decreased in *Sfp1*^{+/-} mice (Figure 7B).

We wondered whether PU.1 is required at the cell-autonomous level for the generation of CD209a⁺ moDCs. We adoptively

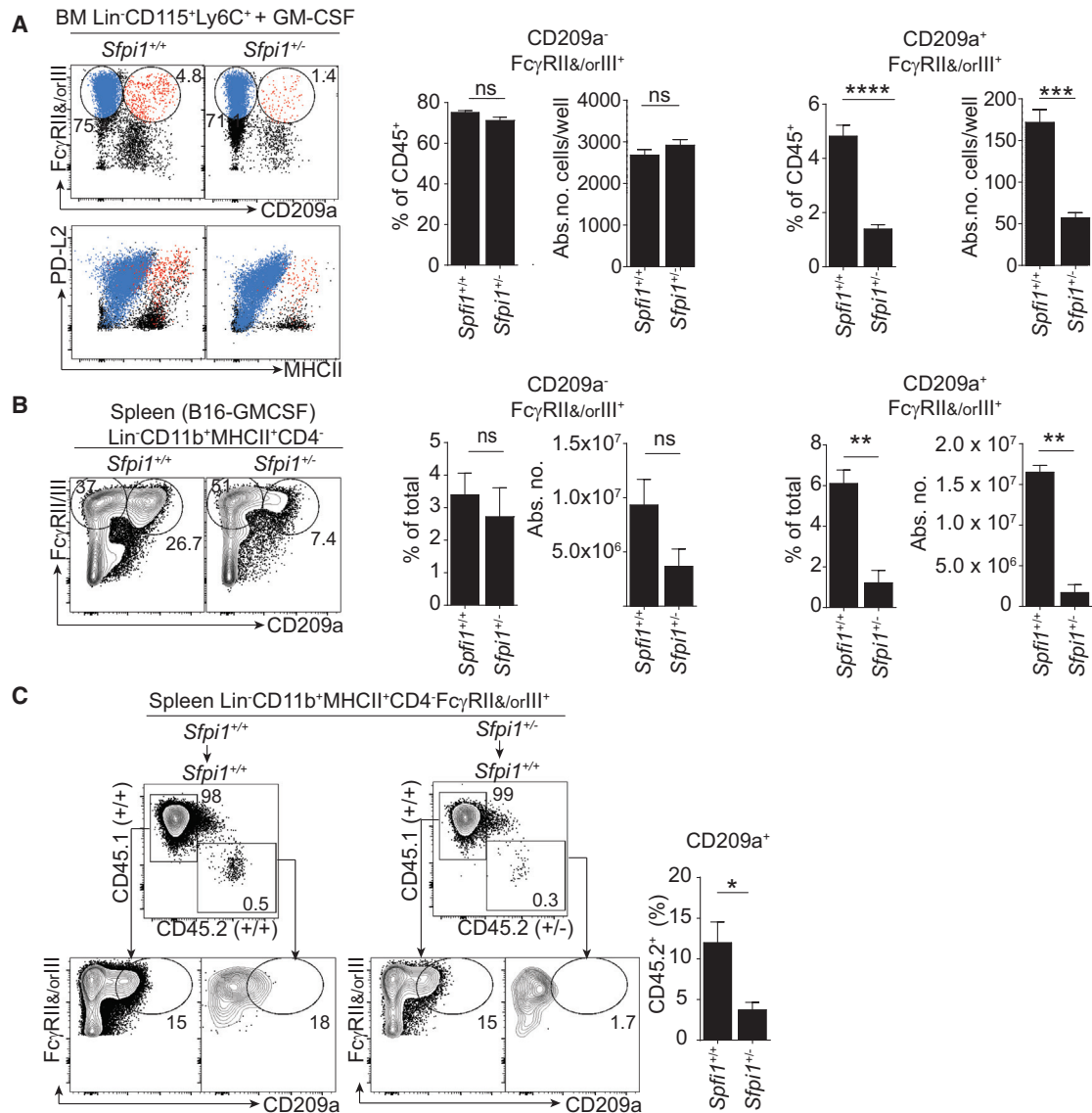


Figure 7. PU.1 Promotes the Generation of GM-CSF-Dependent PD-L2⁺CD209a⁺ moDCs

(A) FcγRII and/or FcγRIII and CD209a expression in GM-CSF culture of BM Lin⁺CD115⁺Ly6C⁺ cells from *Sfp1*^{+/+} or *Sfp1*^{+/-} mice. FcγRII⁺ and/or FcγRIII⁺ CD209a⁻ (blue) and FcγRII⁺ and/or FcγRIII⁺CD209a⁺ (red) cells are overlaid on flow cytometry staining of PDL2 (CD273) and MHCII. The percentage and absolute number of DAPI⁻CD45⁺ cells of each indicated population of *Sfp1*^{+/+} or *Sfp1*^{+/-} BM are shown. Data represent two similar experiments.

(B) Quantification of FcγRII⁺ and/or FcγRIII⁺CD209a⁻ and FcγRII⁺ and/or FcγRIII⁺CD209a⁺ cells in Lin⁺CD11b⁺MHCII⁺CD4⁻ splenocytes from B16-GM-CSF-bearing *Sfp1*^{+/+} or *Sfp1*^{+/-} mice. Data represent six mice.

(C) PU.1 promotes the generation of CD209a⁺ moDCs by a cell-intrinsic mechanism. Shown is the adoptive transfer of CD45.2⁺ *Sfp1*^{+/+} or *Sfp1*^{+/-} BM into B16-GM-CSF-engrafted CD45.1⁺ congenic recipients, as well as CD209a and FcγRII and/or FcγRIII expression on Lin⁺CD11b⁺MHCII⁺CD4⁻ cells of recipient CD45.1⁺ or donor CD45.2⁺ *Sfp1*^{+/+} or *Sfp1*^{+/-} BM. The percentage of CD209a⁺ cells inside the donor Lin⁺CD11b⁺MHCII⁺CD4⁻ FcγRII⁺ and/or FcγRIII⁺CD45.2⁺ cells is quantified (n = 3 mice per group in two identical experiments). Data represent the mean ± SEM (*p < 0.05, **p < 0.005, ***p < 0.0005; Student's t test). Please also refer to Figure S7.

transferred *Sfp1*^{+/+} or *Sfp1*^{+/-} CD45.2⁺ BM into CD45.1⁺ B16-GM-CSF-injected recipients. Unlike *Sfp1*^{+/+} BM, *Sfp1*^{+/-} BM did not generate CD209a⁺ moDCs (Figure 7C). Control populations such as B cells and granulocytes were generated as efficiently upon transfer of either *Sfp1*^{+/+} or *Sfp1*^{+/-} BM (Figure S7B). We conclude that PU.1 selectively controls the differentiation of GM-CSF-dependent CD209a⁺ moDCs by a cell-intrinsic mechanism.

DISCUSSION

Depending on the study, monocyte-derived inflammatory cells (distinct from the cDC lineage) are termed inflammatory macrophages (Bain et al., 2013; Tamoutounour et al., 2012) or moDCs (Cheong et al., 2010; Plantinga et al., 2013; Zigmond et al., 2012). Here, we report that distinct monocyte subsets give rise to iNOS⁺ inflammatory macrophages and CD209a⁺ moDCs.

Indeed, we have shown that a subset of monocytes (R2; CCR2 dependent and not labeled in *Zbtb46^{Cre} x Rosa^{lsYFP}* mice) contain MHCII⁺ cells that are distinct from BTBD4⁺ pre-DCs. These cells develop into CD209a⁺ moDCs upon exposure to GM-CSF both in vitro and in vivo. Conversely, MHCII[−] monocytes (R1) possess the progenitor function for iNOS⁺ inflammatory macrophages. This supports the view that inflammatory macrophages and moDCs are ontogenically distinct populations. In support of this hypothesis, fate mapping of iNOS⁺ inflammatory macrophages did not show an efficient conversion to the moDC phenotype. In addition, single-cell analysis of monocytes (R2; CD11c[−]) identified a mixed transcriptional program characterized by the expression of MHCII genes (downstream activation of CIITA by pI promoter) and DC-related genes such as *Flt3*, *Cd209a*, or *Kmo*, for example. These cells might originate from cMoPs (through *Flt3* acquisition), from CDPs (via loss of DC-specific commitment), or from earlier myeloid-primed progenitors (LMPP or GMPs). Additional experiments are needed to address this. Of note, we have shown that R3 cells (CD11c⁺Flt3⁺CD115⁺BTBD4⁺SiglecH[−]Ly6C⁺) aligning with previously described cDC2-committed pre-cDCs (pre-DC2s) (Schlitzer et al., 2015; Tussiwand et al., 2015) are diverse in terms of MHCII or CD209a expression, for example. The functional relevance of pre-DC2 heterogeneity for the generation of multiple cDC2 subsets (Lewis et al., 2011; Tussiwand et al., 2015) remains to be addressed.

An important question that arises is the transcriptional mechanism driving the steady-state differentiation of Ly6C⁺ monocytes into a small sub-population with a distinct potential to generate moDCs or inflammatory macrophages. PU.1 is a lineage-determining TF essential for hematopoietic stem cells and has multiple roles in the myeloid lineage (Dakic et al., 2005; DeKoter and Singh, 2000; McKercher et al., 1996; Scott et al., 1994). PU.1 cooperates with multiple other TFs to shape the enhancer landscape of tissue-resident macrophages (Lavin et al., 2014; Norris et al., 2014). Here, we report that *Sfp1* haploinsufficiency promotes the generation of iNOS⁺ macrophages during *L.m.* infection. PU.1-dependent negative regulation of iNOS⁺ macrophages might constitute a regulatory mechanism limiting iNOS-dependent immunopathology. How does PU.1 downregulate the production of iNOS? PU.1 is known to upregulate multiple miRNAs, including miR-146 and miR-155, which in turn negatively regulate innate sensing through the regulation of TRAF6, IRAK4, and STAT1, for example (Ghani et al., 2011; Jurkin et al., 2010). Indeed, Ly6C⁺ monocytes from *mir146^{−/−}* mice are hyper-responsive to microbial stimulation (Etzrodt et al., 2012). Higher amounts of PU.1 might be needed to induce mir146 and limit anti-microbial responses. Further experiments are needed to assess the relevance of miRNAs downstream of PU.1-dependent regulation of innate sensing.

We have found that, in addition to having a regulatory effect on microbicidal iNOS⁺ macrophages, the highest amounts of PU.1 selectively promote the generation of GM-CSF-dependent moDCs in vitro and in vivo. This could be explained by (1) the reduction of moDC precursors (MHCII⁺ R2 monocytes) in naive *Sfp1^{+/-}* mice and (2) an effect on moDC terminal differentiation. In support of the latter, overexpression of PU.1 promotes the differentiation of DC-like cells (Bakri et al., 2005), and inducible

ablation of *Sfp1* prevents the differentiation of DCs (Carotta et al., 2010). In this context, PU.1 cooperation with TFs IRF4 and IRF8 could be relevant to explain the role of PU.1 in moDC differentiation from monocytes. PU.1 can bind to Ets binding sites on its own, but PU.1 also cooperates with IRF4 or IRF8 at Ets-IRF composite response elements called EICEs (Brass et al., 1999). IRF4 is known to be involved in the control of CIITA promoter pI in GM-CSF moDCs or CD11b⁺ DCs (Gao et al., 2013; Tamura et al., 2005; Vander Lugt et al., 2014). In addition, PU.1 might boost the expression of growth factor receptors required for the development of moDCs (e.g., CSFR2A; DeKoter et al., 1998).

In conclusion, our results shed light on the readiness of inflammatory monocyte subsets for distinct and specialized developmental programs activated in inflammatory conditions. Importantly, PU.1 amounts segregate the transcriptional programs of microbicidal iNOS⁺ macrophages or moDCs.

EXPERIMENTAL PROCEDURES

Mice

All mice used were between 6 and 12 weeks old and were matched for age and sex in all experiments. They were maintained under specific-pathogen-free conditions in accordance with the UK Animals (Scientific Procedures) Act of 1986.

Cell Isolation and Fluorescence-Activated Cell Sorting

For preparation of BM cell suspensions, the bones of both hind limbs (two tibia and two femurs) were flushed with ice-cold fluorescence-activated cell sorting (FACS) buffer (PBS (Life technologies) with 1% BSA (Apollo Scientific Ltd) and 2 mM EDTA (Life Technologies)). Spleens were collected, cut into small pieces, and incubated with collagenase D (Roche) and DNaseI (Roche) in Hank's balanced salt solution (GE Healthcare) and 5% fetal bovine serum (Life technologies) for 20 min; they were further macerated through 100 μ m cell strainers (BD Falcon). Red blood cells were lysed with 2 ml of ACK lysis buffer (Life Technologies), incubated for 2 min at room temperature, and then diluted with FACS buffer. After centrifugation, cells were either re-suspended in an antibody cocktail in FACS buffer or permeabilized and fixed for intracellular staining and analyzed by flow cytometry with FlowJo software (TreeStar). For cell sorting, see Supplemental Experimental Procedures.

In Vitro GM-CSF Cultures

Total BM or 10⁴ sorted Ly6C^{hi}CD115⁺ monocytes (total or subsets R1–R3) were cultured in 20 ng/ml of GM-CSF in complete RPMI with 6,000 live MS-5 cells as “feeders,” which were plated on the same day. Analyzed cells were pre-gated to be DAPI[−] and CD45⁺.

In Vitro *L.m.* Infections

Primary cells infected with *L.m.* were in vivo cultured overnight at an MOI of 0.01, 0.1, 1, or 10 (as indicated in Figure 5) in complete RPMI medium supplemented with macrophage colony-stimulating factor (M-CSF, 20 ng/ml; Peprotech), GM-CSF (3 ng/ml; Peprotech), and human Flt3L (100 ng/ml; CellDex). BMDMs were derived by culture of whole BM in RPMI supplemented with culture medium from L-929 cells.

B16-GM-CSF Tumor Experiments

B16-GM-CSF tumor cells were checked for viability with Trypan Blue, and 1.5 \times 10⁵ to 3 \times 10⁵ live cells were injected subcutaneously (see Supplemental Experimental Procedures).

Infection

4 \times 10³ to 5 \times 10³ WT colony-forming units (CFU) (*Listeria*) or 10⁶ Δ ActA mutant CFU of *L.m.* (Δ ActA *Listeria*) were injected intravenously into sterile PBS (see Supplemental Experimental Procedures).

Microarray

Cells sorted by flow cytometry were collected in complete RPMI and pelleted, lysed in Buffer RLT (RNeasy Kit, QIAGEN), and frozen at -80°C until they were processed for RNA. The NuGEN Ovation Pico WTA V2 Kit was used to process 1 ng RNA per sample into cDNA amplified by single-primer isothermal amplification. The Encore Biotin Module (NuGEN) was used to fragment and label the cDNA with biotin. Hybridization cocktails were prepared as recommended by NuGEN and hybridized to Affymetrix Mouse Gene 1.0 ST arrays overnight. Arrays were washed and stained with Affymetrix Fluidics Station FS450 and the GeneChip Hybridization, Wash, and Stain Kit and scanned by the GeneChip Scanner 3000 7G with Autoloader. Raw data files (DAT and CEL) were generated in Affymetrix GeneChip Command Console software and are available at GEO: GSE90471. Data were analyzed with GenePattern software (Broad Institute), and pre-DC and CDP datasets were obtained from public databases.

t-SNE Analysis

Single-cell analysis using the t-SNE algorithm was done on flow cytometry data in the online platform provided by Cytobank (see [Supplemental Experimental Procedures](#)).

Single-Cell qPCR

Single cells were sorted by flow cytometry, cDNA was amplified with the CellsDirect One-Step qRT-PCR Kit (ThermoFisher), and qPCR was run on a BioMark HD (Fluidigm) with the help of Taqman probes (Life Technologies) for the genes indicated in [Figure 2](#). The 45 targeted genes were analyzed against an average of three housekeeping genes: *Hprt*, *ActB*, and *Gapdh*. Analysis was done with the help of Gene-E software (Broad Institute) (see [Supplemental Experimental Procedures](#)).

qPCR

qPCR was carried out in duplicate for samples sorted from three independent sorting experiments. Primers used for testing *Zbtb46* were 5'-AGAGAG CACATGAAGCGACA-3' (forward) and 5'-CTGGCTGCAGACATGAACAC-3' (reverse). Results were normalized against β -actin: 5'-ATGCTCCCGGG CTGTAT-3' (forward) and 5'-CATAGGAGTCCTTCTGACCCATTC-3' (reverse).

Adoptive Transfer

For adoptive transfer of cells sorted by flow cytometry, 3.3×10^5 cells of each population were collected in complete RPMI, centrifuged, resuspended in 120 μl of RPMI alone, and injected intravenously into each CD45.1⁺ congenic recipient. For whole-BM transfers, single-cell suspensions of BM were depleted of red blood cells by exposure to RBC lysis buffer (Life technologies) and counted. 40×10^6 whole-BM cells from *Sfp1*^{+/+} or *Sfp1*^{+/-} mice were transferred into B16-GM-CSF-treated congenic CD45.1⁺ mice on day 9 and analyzed on day 11 after tumor injection. For *L.m.*-infected recipients, 20×10^6 whole-BM cells were transferred into congenic CD45.1⁺ recipients 2 hr before intravenous *L.m.* infection.

Statistical Analysis

Data were analyzed for statistical significance by unpaired Student's t tests. Differences were considered significant at $p < 0.05$ (* $p < 0.05$; ** $p < 0.005$; *** $p < 0.0005$; **** $p < 0.00005$; ns, non-significant).

ACCESSION NUMBERS

The accession number for the microarray data reported in this paper is GEO: GSE90471.

SUPPLEMENTAL INFORMATION

Supplemental Information includes Supplemental Experimental Procedures, seven figures, and one table and can be found with this article online at <http://dx.doi.org/10.1016/j.immuni.2016.12.001>.

AUTHOR CONTRIBUTIONS

S.M. performed most of the experiments (with help from R.P., D.M., and G.A. for some) and designed the figures. T.P. performed the single-cell multiplex

qPCR; R.G. provided expertise for the design of these experiments. J.D.A., S.H., and A.-M.L.-D. provided help for the analysis of MHCII expression and its transcriptional regulation and performed some experiments addressing the role of CIITA. J.L., M.C.N., and M.P.L. provided tools and expertise for the analysis of *Zbtb46* expression and the fate mapping of *Zbtb46*-expressing cells. G.L., A.B., and F.G. provided reagents and expertise with the fate mapping of iNOS-expressing cells. J.Y.H and S.A.Q provided reagents and expertise with the B16-GM-CSF melanoma model. E.L.G, E.G.-M, C.E.J.-G., E.G.-P., H.G., and F.G. provided mice models, expertise for the analysis of monocyte populations, and helpful discussions. The manuscript was written by P.G. and S.M. Experiments were designed by P.G. in collaboration with S.M.

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